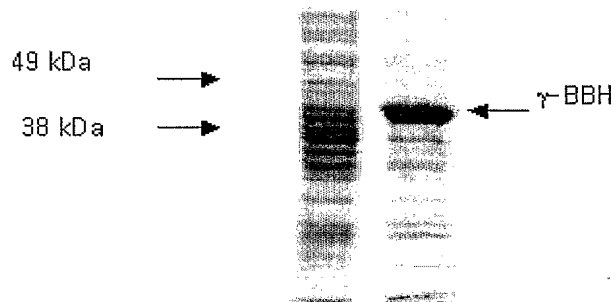
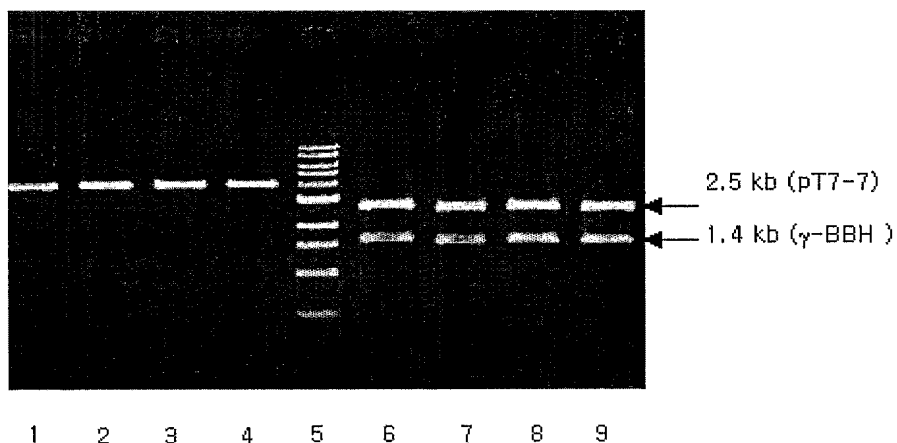


1/3
1



Lane 1 : Protein molecular size marker,
Lane 2 : E.coli BL21 w/o g -BBH gene,
Lane 3 : E.coli BL21 w/ g -BBH gene and induced by 1mM IPTG

2



Lane 1~4 : pT7-7 + g-BBH plasmid digested with Nde I
Lane 5: 1kb DNA ladder
Lane 6~9 : pT7-7 + g-BBH plasmid digested with Nde I and Sal I

2/3

3

CLUSTAL W (1.82) multiple sequence alignment

```

Human      -----MACTIQKAEALDGAHLMQILWYDEEESLYPAVWLRDNCPCSDCYLDSAKARK 52
rat        -----MHCAILKAEAYDGAHLMQIFWHDGAESLYPAVWLRDNCQCSDCYLHSAKARK 52
pseudomonas NA IADVRTFPLI SPLASAA SFASGVSVTWADGRVSPFHNLWLRDNCPCGDCVVEVTRQV 60
N.crassa   -----MATAAVQVSVPAVPVGGPDI GYAPDHDKYLARVKRRRENEKLESSLPFG---- 48
           :      . . .      .      :      :      :      *      :      :

Human      LLVEALDYNIGIKGLIFDRK-KYVITWPDHYSEFQADWLKKRCFSKQARAKLQRELFFP 111
rat        LLEALDYNIRMDDLTFDQK-KYVITWPNGHVSEFEANWLKKRCFSQEARAGLQGEFLFP 111
pseudomonas FLVADVPEDIQVQAVTIGDDGRLVVQWDDGHASAYHPGWLRAHAYDAQSLA--EREAAAP 118
N.crassa   --FPRRLDSDLVWDGNTLAETVDWTVRLTEEAIDEIEAALRHFKSLNKPLGVINQETFFLP 107
           :      :      :      :      :      :      :      :      :      :      *

Human      ECQYWGSELQLPTLDFEDVLRVDEHAYKWLSTLKKVGI VRLTGASDKPGEVSKLGKRMGF 171
rat        ECQYWGSELQLPTLNFEDVLRNDDHAYKWLSSLKKVGI VRLTGAADKRGELIKLGKRI GF 171
pseudomonas HKHRWMQQLSLPVYDHGAYMQDDDTLLEWLLAVRDVGLTQLHGVPTEPGAL I PLAKRI SF 178
N.crassa   RLHHTLRSLSHLHHGHGFKYLR--GLPYTSHTREENII IYAGVSSHVAPI RGRQDNQ-H 164
           .      :      *      .      .      .      :      :      *      .      .      .

Human      LYLTFYGHWTQVQDKIDANNVAYTTGKLSFHTDYPALHHPGP-VQLLHC I KQTYTGGDSE 230
rat        LYLTFYGHWTQVQDKIDANNVAYTTGKLSFHTDYPALHHPGP-VQLLHC I KQTYTGGDSE 230
pseudomonas IRESNFGVLFQVRSKADADSNAYTAFNLPLHTDLPTRELQPG-LQFLHCLVNDATGGNST 237
N.crassa   NGHPADYVLAHI KDLSTTVSDYSKI GAPAYTTEKQVFHTDAGDI VALFCLGEAAEGGQSY 224
           .      :      :      :      :      :      :      *      :      :      *      :      :      *      :

Human      IVDGFNYCQKLKKNPQAFQILSS--TFVDFTDIGV-----DYCDFSVQSKHKI I ELDDK 283
rat        IVDGFNYCQKLKKNPQAFQILSS--TFVDFTDIGV-----DYCDFSVQSKHKI I ELDDK 283
pseudomonas FVDGFAIAEALRIEAPAAVRLICE--TPVEFRNK-----DRHSDVACTAPVIALDSS 287
N.crassa   LSSSWKVYNELAAATRPDLVRTLAEPWVADEFGKEGRKFSVRPLLHFQSTAAAAASREAKPE 284
           :      :      :      :      *      *      *      .      :      *      .      .      .

Human      GQVYRINFNNA TRDTIFDVP-VERVQPFYAALKEFVDLMN--SKESKFTFKMNP GDVITF 340
rat        GQVYRINFNNA TRDTVFDVP-IERVQPFYAALKEFVDLMN--SKEYKYTFKMNP GDVITF 340
pseudomonas GEVREIRLANFLR-APFQMD-AQRMPDYVYLAVRRFI QMTR--EPRFCFTRALEAGQLWCF 343
N.crassa   SERLI IQYARRFTGYWGLPRSADIPPI TEAQAEALDALHFTA EKYAYALOFRQGDVQFV 344
           .      :      *      .      :      :      :      *      .      :      :      :      *      :

Human      DNWRLLHGRRSYEAGTEISRHLEGAYAD-----WDVYMS-----RLRI L 379
rat        DNWRLLHGRRSYEAGTEISRHLEGAYAD-----WDVYMS-----RLRI L 379
pseudomonas DNRRYLHARDAFDP-ASGDRHFQGCYVD-----RDELLS-----RI LVL 381
N.crassa   NNLSVFHSRAGFRDEGEKQRLHLYRLWLRDPENAWETPEALKERWERVYGGVSPEREVFP 404
           :      *      :      :      *      .      :      :      :      :      :      :      :      *

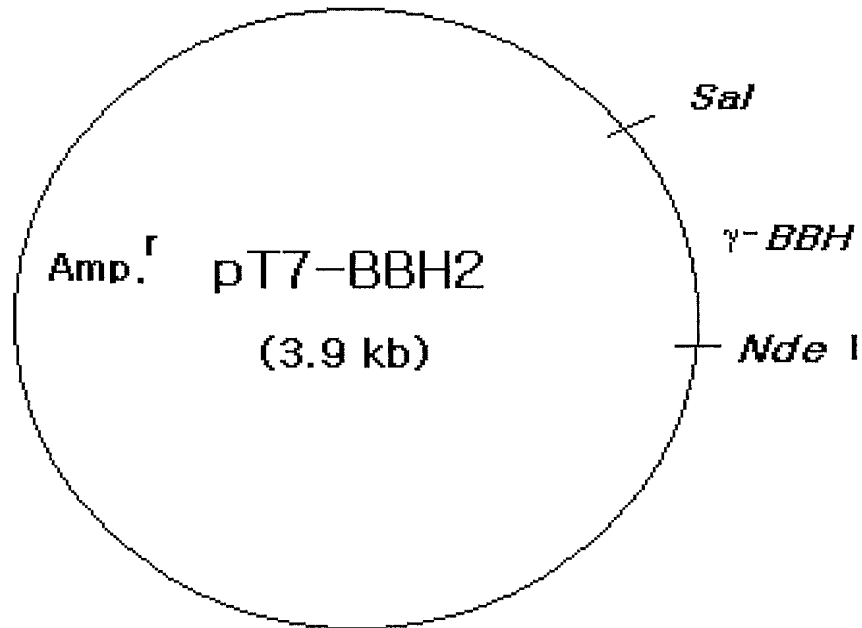
Human      RQRYENG----- 387
rat        RQRYMNG----- 387
pseudomonas QR----- 383
N.crassa   EPQIRASAKGESVGTQGGGGY 425

```

(Sequences were aligned using the European Bioinformatics Institute (EMBL-EBI) sequence analysis program, clustalW.)

3/3

4



5

